

CLAIMS

1. A method of inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain, comprising contacting said PDZ domain with an effective amount of an agent that competes with the binding of the C-terminal region of said cytoplasmic domain of MUC1
5 with said PDZ domain.
2. The method of claim 1, wherein said PDZ domain is ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751, MAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1.
3. The method of claim 1, wherein said agent that competes with binding of said C-
10 terminal region of cytoplasmic domain of MUC1 with said PDZ domain is a peptide of the formula X^1 -aa²-aa¹-aa⁰, wherein aa⁰ is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa² is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa¹ is an amino acid residue and X¹ is a sequence of 0 to 50
15 amino acid residues.
4. The method of claim 3, wherein aa⁰ is V, L, A, I, S or Y and aa² is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E.
5. The method of claim 3, wherein aa²-aa¹-aa⁰ is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.
- 20 6. The method of claim 3, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.
7. The method of claim 3, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19
25 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.
8. The method of claim 3, wherein the amino terminus of X¹ comprises X²-X³, wherein X² is a transmembrane transporter peptide sequence and X³ is an optional linker sequence.

9. The method of claim 8, wherein X^2 is a sequence selected from SEQ ID NO 97 through SEQ ID NO: 127.
10. The method of claim 9, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.
- 5 11. A method of inhibiting the binding of the cytoplasmic domain of MUC1 to one or more PDZ proteins within a MUC1 expressing cancer cell comprising contacting said MUC1 expressing cancer cell with an effective amount of an agent that competes with the binding of the C-terminal region of said cytoplasmic domain of MUC1 with said PDZ protein.
- 10 12. The method of claim 11, wherein one or more PDZ proteins is/are selected from the group consisting of ZO-1 d2, SIP1 d1, LIM MYSTIQUE, AIPC, KIAA0751, MAST2, and PRIL-16 d1.
- 15 13. The method of claim 11, wherein said agent that competes with binding of said C-terminal region of cytoplasmic domain of MUC1 with said one or more PDZ proteins is a peptide of the formula X^1 -aa²-aa¹-aa⁰, wherein aa⁰ is a hydrophobic aliphatic amino acid residue, aa² is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa¹ is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.
- 20 14. The method of claim 13, wherein aa⁰ is V, L, A, I, S or Y and aa² is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E.
15. The method of claim 13, wherein aa²-aa¹-aa⁰ is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.
- 25 16. The method of claim 13, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.
17. The method of claim 13, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

18. The method of claim 13, wherein the amino terminus of X^1 comprises X^2 - X^3 , wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.
19. The method of claim 18, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.
- 5 20. The method of claim 19, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.
21. A method of enhancing the sensitivity of MUC1-expressing cancer cells to chemotherapeutic agents comprising contacting said MUC1-expressing cancer with an effective amount of a peptide of the formula X^1 - aa^2 - aa^1 - aa^0 , wherein aa^0 is a hydrophobic
10 aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.
22. The method of claim 21, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y,
15 W, Q, N, S, T, R, K, D or E .
23. The method of claim 21, wherein aa^2 - aa^1 - aa^0 is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.
24. The method of claim 21, wherein the carboxy-terminus of said peptide of formula X^1 - aa^2 - aa^1 - aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8 or 9 amino acid residues of a nine
20 amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.
25. The method of claim 21, wherein the carboxy-terminus of said peptide of formula X^1 - aa^2 - aa^1 - aa^0 comprises the carboxy-terminal 4, 5 6, 7, 8, 9,10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.
26. The method of claim 21, wherein the amino terminus of X^1 comprises X^2 - X^3 , wherein
25 X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.
27. The method of claim 26, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

28. The method of claim 27, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.

29. A method of killing MUC1-expressing cancer cells comprising contacting said MUC1-expressing cancer cells with an effective amount of a chemotherapeutic agent and an effective amount of a peptide of the formula X^1 -aa²-aa¹-aa⁰, wherein aa⁰ is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic amino acid residue, aa² is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa¹ is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

30. The method of claim 29, wherein said chemotherapeutic agent is a DNA-interactive agent, a tubulin interactive agent, and an antimetabolite chemotherapeutic agent.

31. The method of claim 29, wherein aa⁰ is V, L, A, I, S or Y and aa² is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E.

32. The method of claim 29, wherein aa²-aa¹-aa⁰ is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

33. The method of claim 29, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5, 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

34. The method of claim 29, wherein the carboxy-terminus of said peptide of formula X^1 -aa²-aa¹-aa⁰ comprises the carboxy-terminal 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

35. The method of claim 29, wherein the amino terminus of X^1 comprises X^2 - X^3 , wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

36. The method of claim 35, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

37. The method of claim 36, wherein X^2 is SEQ ID NO: 98, SEQ ID NO: 104 or SEQ ID NO: 119.

38. A method of killing MUC1-expressing cancer cells comprising contacting said MUC1-expressing cancer cells with an effective amount of a chemotherapeutic agent and an effective amount of an agent that inhibits the binding of the carboxy-terminal of the cytoplasmic tail of MUC1 with the PDZ domain of KIAA0751.

5 39. The method of claim 38, wherein said chemotherapeutic agent is a DNA-interactive agent, a tubulin interactive agent, and an antimetabolite chemotherapeutic agent.

40. The method of claim 38, wherein said agent that inhibits the binding of the carboxy-terminal of the cytoplasmic tail of MUC1 with the PDZ domain of KIAA0751 is a peptide of the formula $X^1\text{-aa}^2\text{-aa}^1\text{-aa}^0$, wherein aa^0 is a hydrophobic aliphatic amino acid residue or a hydrophobic aromatic acid residue, aa^2 is a hydrophobic aliphatic amino acid residue, hydrophobic aromatic amino acid residue, polar amino acid residue, basic amino acid residue or an acidic amino acid residue, aa^1 is an amino acid residue and X^1 is a sequence of 0 to 50 amino acid residues.

41. The method of claim 40, wherein aa^0 is V, L, A, I, S or Y and aa^2 is V, L, A, I, F, Y, W, Q, N, S, T, R, K, D or E.

42. The method of claim 40, wherein $\text{aa}^2\text{-aa}^1\text{-aa}^0$ is a sequence selected from SEQ ID NO: 1 through SEQ ID NO: 40.

43. The method of claim 40, wherein the carboxy-terminus of said peptide of formula $X^1\text{-aa}^2\text{-aa}^1\text{-aa}^0$ comprises the carboxy-terminal 4, 5, 6, 7, 8 or 9 amino acid residues of a nine amino acid residue sequence selected from SEQ ID NO: 41 through SEQ ID NO: 94.

44. The method of claim 40, wherein the carboxy-terminus of said peptide of formula $X^1\text{-aa}^2\text{-aa}^1\text{-aa}^0$ comprises the carboxy-terminal 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acid residues of SEQ ID NO: 95 or SEQ ID NO: 96.

45. The method of claim 40, wherein the amino terminus of X^1 comprises $X^2\text{-X}^3$, wherein X^2 is a transmembrane transporter peptide sequence and X^3 is an optional linker sequence.

46. The method of claim 45, wherein X^2 is a sequence selected from SEQ ID NO: 97 through SEQ ID NO: 127.

47. The method of claim 45, wherein X^2 is SEQ ID NO: 102, SEQ ID NO: 108 or SEQ ID NO: 119.